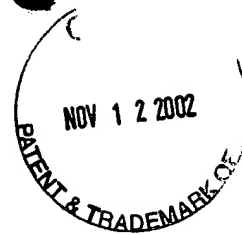


APPENDIX C



lalign output for HopE vs. SEQ ID NO:809

[ISREC-Server] Date: Tue Nov 5 0:34:27 MET 2002

./wwwtmp/lalign/.27078.1.seq : 239 aa

ALIGN calculates a global alignment of two sequences

version 2.0uPlease cite: Myers and Miller, CABIOS (1989) 4:11-17

hopE 239 aa vs.

809 148 aa

scoring matrix: BLOSUM50, gap penalties: -14/-4

47.3% identity; Global alignment score: 309

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```

                                10      20      30
HopE  -----EGDGVYIGTNYQLGQARLNSNIYNTGDCTGSVVGCPP
                                :
809    MEIIKKFVALGLLSAVLSSSLAEGDGVYIGTNYQLGQARLNSNIYNTGDCTGSVVGCPP
                                10      20      30      40      50      60

      40      50      60      70      80      90
HopE    GLTANKHNPGGTNINWHSKYANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDY
      :
809    GLTANKHNPGGTNINWHSKYANGALNGFGLNVGYKKFFQFKSLDMTSKWFGFRVYGLFDY
      70      80      90      100     110     120

      100     110     120     130     140     150
HopE    GHADLGKQVYAPNKIQLDMVSWGVSDDLADIIDKDNASFGIFGGVAIGGNTWKSSAANY
      :
809    GHADLGKQVYAPNKIQLDMVSWGVS-----
      130     140

      160     170     180     190     200     210
HopE    WKEQIIIEAKGPDVCTPTYCNPAPYSTNTSTVAFQVWLNFGVRANIYKHNGVEFGVRVPL
      .:
809    -----IC-----

      220     230
HopE    LINKFLSAGPNATNLYYHLKRD
809    -----

```